

SEQUENCE LISTING

<110> Piddington, Christopher S.
 Sheppard, Paul O.
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<120> ADIPOCYTE COMPLEMENT RELATED PROTEIN
 HOMOLOG ZACRP5

<130> 99-10C1

<150> US 09/573,733

<151> 2000-05-18

<150> US 60/136,292

<151> 1999-05-27

<160> 15

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 759

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(759)

<400> 1

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Met Ala Ala Pro Ala Leu Leu Leu Leu Ala Leu Leu Leu Pro Val Gly	
1 5 10 15	
gcc tgg ccc ggg ctg ccc agg agg ccc tgt gtg cac tgc tgc cgc ccg	96
Ala Trp Pro Gly Leu Pro Arg Arg Pro Cys Val His Cys Cys Arg Pro	
20 25 30	
gcc tgg ccc cct gga ccc tat gcc cgg gtg agt gac agg gac ctg tgg	144
Ala Trp Pro Pro Gly Pro Tyr Ala Arg Val Ser Asp Arg Asp Leu Trp	
35 40 45	
agg ggg gac ctg tgg agg ggg ctg cct cga gta cgg ccc act ata aac	192
Arg Gly Asp Leu Trp Arg Gly Leu Pro Arg Val Arg Pro Thr Ile Asn	
50 55 60	
atc gaa atc ctc aaa ggt gag aag ggt gag gcc ggc gtc cga ggt cgg	240
Ile Glu Ile Leu Lys Gly Glu Lys Gly Glu Ala Gly Val Arg Gly Arg	
65 70 75 80	
gcc ggc agg agc ggg aaa gag ggg ccg cca ggc gcc cgg ggc ctg cag	288
Ala Gly Arg Ser Gly Lys Glu Gly Pro Pro Gly Ala Arg Gly Leu Gln	
85 90 95	
ggc cgc aga ggc cag aag ggg cag gtg ggg ccg ccg ggc gcc gcg tgc	336
Gly Arg Arg Gly Gln Lys Gly Gln Val Gly Pro Pro Gly Ala Ala Cys	
100 105 110	
cga cgt gcc tac gcc gcc ttc tcc gtg ggc cgg cgc gag ggc ctg cac	384
Arg Arg Ala Tyr Ala Ala Phe Ser Val Gly Arg Arg Glu Gly Leu His	
115 120 125	
agc tcc gac cac ttc cag gcg gtg ccc ttc gac acg gag ctg gtg aac	432
Ser Ser Asp His Phe Gln Ala Val Pro Phe Asp Thr Glu Leu Val Asn	
130 135 140	

ctg gac ggc gcc ttc gac ctg gcc gcg ggc cgc ttc ctc tgc acg gtg 480
 Leu Asp Gly Ala Phe Asp Leu Ala Ala Gly Arg Phe Leu Cys Thr Val
 145 150 155 160
 ccc ggc gtc tac ttc ctc agc ctc aac gtg cac acc tgg aac tac aag 528
 Pro Gly Val Tyr Phe Leu Ser Leu Asn Val His Thr Trp Asn Tyr Lys
 165 170 175
 gag acc tac ctg cac atc atg ctg aac cgg cgg ccc gcg gcc gtg ctc 576
 Glu Thr Tyr Leu His Ile Met Leu Asn Arg Arg Pro Ala Ala Val Leu
 180 185 190
 tac gcg cag ccc agc gag cgc agc gtc atg cag gcc cag agc ctg atg 624
 Tyr Ala Gln Pro Ser Glu Arg Ser Val Met Gln Ala Gln Ser Leu Met
 195 200 205
 ctg ctg ctg gcg gcg ggc gac gcc gtc tgg gtg cgc atg ttc cag cgc 672
 Leu Leu Leu Ala Ala Gly Asp Ala Val Trp Val Arg Met Phe Gln Arg
 210 215 220
 gac cgg gac aac gcc atc tac ggc gag cac gga gac ctc tac atc acc 720
 Asp Arg Asp Asn Ala Ile Tyr Gly Glu His Gly Asp Leu Tyr Ile Thr
 225 230 235 240
 ttc agc ggc cac ctg gtc aag ccg gcc gcc gag ctg tag 759
 Phe Ser Gly His Leu Val Lys Pro Ala Ala Glu Leu *
 245 250

<210> 2
 <211> 252
 <212> PRT
 <213> Homo sapiens

<400> 2
 Met Ala Ala Pro Ala Leu Leu Leu Leu Ala Leu Leu Leu Pro Val Gly
 1 5 10 15
 Ala Trp Pro Gly Leu Pro Arg Arg Pro Cys Val His Cys Cys Arg Pro
 20 25 30
 Ala Trp Pro Pro Gly Pro Tyr Ala Arg Val Ser Asp Arg Asp Leu Trp
 35 40 45
 Arg Gly Asp Leu Trp Arg Gly Leu Pro Arg Val Arg Pro Thr Ile Asn
 50 55 60
 Ile Glu Ile Leu Lys Gly Glu Lys Gly Glu Ala Gly Val Arg Gly Arg
 65 70 75 80
 Ala Gly Arg Ser Gly Lys Glu Gly Pro Pro Gly Ala Arg Gly Leu Gln
 85 90 95
 Gly Arg Arg Gly Gln Lys Gly Gln Val Gly Pro Pro Gly Ala Ala Cys
 100 105 110
 Arg Arg Ala Tyr Ala Ala Phe Ser Val Gly Arg Arg Glu Gly Leu His
 115 120 125
 Ser Ser Asp His Phe Gln Ala Val Pro Phe Asp Thr Glu Leu Val Asn
 130 135 140
 Leu Asp Gly Ala Phe Asp Leu Ala Ala Gly Arg Phe Leu Cys Thr Val
 145 150 155 160
 Pro Gly Val Tyr Phe Leu Ser Leu Asn Val His Thr Trp Asn Tyr Lys
 165 170 175
 Glu Thr Tyr Leu His Ile Met Leu Asn Arg Arg Pro Ala Ala Val Leu
 180 185 190
 Tyr Ala Gln Pro Ser Glu Arg Ser Val Met Gln Ala Gln Ser Leu Met
 195 200 205
 Leu Leu Leu Ala Ala Gly Asp Ala Val Trp Val Arg Met Phe Gln Arg
 210 215 220
 Asp Arg Asp Asn Ala Ile Tyr Gly Glu His Gly Asp Leu Tyr Ile Thr
 225 230 235 240

Phe Ser Gly His Leu Val Lys Pro Ala Ala Glu Leu
 245 250

<210> 3
 <211> 281
 <212> PRT
 <213> Homo sapiens

<400> 3
 Met Gly Ser Arg Gly Gln Gly Leu Leu Leu Ala Tyr Cys Leu Leu Leu
 1 5 10 15
 Ala Phe Ala Ser Gly Leu Val Leu Ser Arg Val Pro His Val Gln Gly
 20 25 30
 Glu Gln Gln Glu Trp Glu Gly Thr Glu Glu Leu Pro Ser Pro Pro Asp
 35 40 45
 His Ala Glu Arg Ala Glu Glu Gln His Glu Lys Tyr Arg Pro Ser Gln
 50 55 60
 Asp Gln Gly Leu Pro Ala Ser Arg Cys Leu Arg Cys Cys Asp Pro Gly
 65 70 75 80
 Thr Ser Met Tyr Pro Ala Thr Ala Val Pro Gln Ile Asn Ile Thr Ile
 85 90 95
 Leu Lys Gly Glu Lys Gly Asp Arg Gly Asp Arg Gly Leu Gln Gly Lys
 100 105 110
 Tyr Gly Lys Thr Gly Ser Ala Gly Ala Arg Gly His Thr Gly Pro Lys
 115 120 125
 Gly Gln Lys Gly Ser Met Gly Ala Pro Gly Glu Arg Cys Lys Ser His
 130 135 140
 Tyr Ala Ala Phe Ser Val Gly Arg Lys Lys Pro Met His Ser Asn His
 145 150 155 160
 Tyr Tyr Gln Thr Val Ile Phe Asp Thr Glu Phe Val Asn Leu Tyr Asp
 165 170 175
 His Phe Asn Met Phe Thr Gly Lys Phe Tyr Cys Tyr Val Pro Gly Leu
 180 185 190
 Tyr Phe Phe Ser Leu Asn Val His Thr Trp Asn Gln Lys Glu Thr Tyr
 195 200 205
 Leu His Ile Met Lys Asn Glu Glu Glu Val Val Ile Leu Phe Ala Gln
 210 215 220
 Val Gly Asp Arg Ser Ile Met Gln Ser Gln Ser Leu Met Leu Glu Leu
 225 230 235 240
 Arg Glu Gln Asp Gln Val Trp Val Arg Leu Tyr Lys Gly Glu Arg Glu
 245 250 255
 Asn Ala Ile Phe Ser Glu Glu Leu Asp Thr Tyr Ile Thr Phe Ser Gly
 260 265 270
 Tyr Leu Val Lys His Ala Thr Glu Pro
 275 280

<210> 4
 <211> 244
 <212> PRT
 <213> Homo sapiens

<400> 4
 Met Leu Leu Leu Gly Ala Val Leu Leu Leu Leu Ala Leu Pro Gly His
 1 5 10 15
 Asp Gln Glu Thr Thr Thr Gln Gly Pro Gly Val Leu Leu Pro Leu Pro
 20 25 30
 Lys Gly Ala Cys Thr Gly Trp Met Ala Gly Ile Pro Gly His Pro Gly
 35 40 45
 His Asn Gly Ala Pro Gly Arg Asp Gly Arg Asp Gly Thr Pro Gly Glu
 50 55 60
 Lys Gly Glu Lys Gly Asp Pro Gly Leu Ile Gly Pro Lys Gly Asp Ile
 65 70 75 80
 Gly Glu Thr Gly Val Pro Gly Ala Glu Gly Pro Arg Gly Phe Pro Gly
 85 90 95

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Ile Gln Gly Arg Lys Gly Glu Pro Gly Glu Gly Ala Tyr Val Tyr Arg
      100      105      110
Ser Ala Phe Ser Val Gly Leu Glu Thr Tyr Val Thr Ile Pro Asn Met
      115      120      125
Pro Ile Arg Phe Thr Lys Ile Phe Tyr Asn Gln Gln Asn His Tyr Asp
      130      135      140
Gly Ser Thr Gly Lys Phe His Cys Asn Ile Pro Gly Leu Tyr Tyr Phe
145      150      155      160
Ala Tyr His Ile Thr Val Tyr Met Lys Asp Val Lys Val Ser Leu Phe
      165      170      175
Lys Lys Asp Lys Ala Met Leu Phe Thr Tyr Asp Gln Tyr Gln Glu Asn
      180      185      190
Asn Val Asp Gln Ala Ser Gly Ser Val Leu Leu His Leu Glu Val Gly
      195      200      205
Asp Gln Val Trp Leu Gln Val Tyr Gly Glu Gly Glu Arg Asn Gly Leu
      210      215      220
Tyr Ala Asp Asn Asp Asn Asp Ser Thr Phe Thr Gly Phe Leu Leu Tyr
225      230      235      240
His Asp Thr Asn

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<210> 5
<211> 243
<212> PRT
<213> Homo sapiens

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<400> 5
Met Arg Pro Leu Leu Val Leu Leu Leu Leu Gly Leu Ala Ala Gly Ser
 1      5      10      15
Pro Pro Leu Asp Asp Asn Lys Ile Pro Ser Leu Cys Pro Gly His Pro
      20      25      30
Gly Leu Pro Gly Thr Pro Gly His His Gly Ser Gln Gly Leu Pro Gly
      35      40      45
Arg Asp Gly Arg Asp Gly Arg Asp Gly Ala Pro Gly Ala Pro Gly Glu
      50      55      60
Lys Gly Glu Gly Gly Arg Pro Gly Leu Pro Gly Pro Arg Gly Asp Pro
65      70      75      80
Gly Pro Arg Gly Glu Ala Gly Pro Ala Gly Pro Thr Gly Pro Ala Gly
      85      90      95
Glu Cys Ser Val Pro Pro Arg Ser Ala Phe Ser Ala Lys Arg Ser Glu
      100      105      110
Ser Arg Val Pro Pro Pro Ser Asp Ala Pro Leu Pro Phe Asp Arg Val
      115      120      125
Leu Val Asn Glu Gln Gly His Tyr Asp Ala Val Thr Gly Lys Phe Thr
      130      135      140
Cys Gln Val Pro Gly Val Tyr Tyr Phe Ala Val His Ala Thr Val Tyr
145      150      155      160
Arg Ala Ser Leu Gln Phe Asp Leu Val Lys Asn Gly Glu Ser Ile Ala
      165      170      175
Ser Phe Phe Gln Phe Phe Gly Gly Trp Pro Lys Pro Ala Ser Leu Ser
      180      185      190
Gly Gly Ala Met Val Arg Leu Glu Pro Glu Asp Gln Val Trp Val Gln
      195      200      205
Val Gly Val Gly Asp Tyr Ile Gly Ile Tyr Ala Ser Ile Lys Thr Asp
      210      215      220
Ser Thr Phe Ser Gly Phe Leu Val Tyr Ser Asp Trp His Ser Ser Pro
225      230      235      240
Val Phe Ala

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<210> 6
<211> 245
<212> PRT
<213> Homo sapiens

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<400> 6

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Met Asp Val Gly Pro Ser Ser Leu Pro His Leu Gly Leu Lys Leu Leu
1      5      10      15
Leu Leu Leu Leu Leu Ala Leu Arg Gly Gln Ala Asn Thr Gly Cys
20     25     30
Tyr Gly Ile Pro Gly Met Pro Gly Leu Pro Gly Ala Pro Gly Lys Asp
35     40     45
Gly Tyr Asp Gly Leu Pro Gly Pro Lys Gly Glu Pro Gly Ile Pro Ala
50     55     60
Ile Pro Gly Ile Arg Gly Pro Lys Gly Gln Lys Gly Glu Pro Gly Leu
65     70     75     80
Pro Gly His Pro Gly Lys Asn Gly Pro Met Gly Pro Pro Gly Met Pro
85     90     95
Gly Val Pro Gly Pro Met Gly Ile Pro Gly Glu Pro Gly Glu Glu Gly
100    105    110
Arg Tyr Lys Gln Lys Phe Gln Ser Val Phe Thr Val Thr Arg Gln Thr
115    120    125
His Gln Pro Pro Ala Pro Asn Ser Leu Ile Arg Phe Asn Ala Val Leu
130    135    140
Thr Asn Pro Gln Gly Asp Tyr Asp Thr Ser Thr Gly Lys Phe Thr Cys
145    150    155    160
Lys Val Pro Gly Leu Tyr Tyr Phe Val Tyr His Ala Ser His Thr Ala
165    170    175
Asn Leu Cys Val Leu Leu Tyr Arg Ser Gly Val Lys Val Val Thr Phe
180    185    190
Cys Gly His Thr Ser Lys Thr Asn Gln Val Asn Ser Gly Gly Val Leu
195    200    205
Leu Arg Leu Gln Val Gly Glu Val Trp Leu Ala Val Asn Asp Tyr
210    215    220
Tyr Asp Met Val Gly Ile Gln Gly Ser Asp Ser Val Phe Ser Gly Phe
225    230    235    240
Leu Leu Phe Pro Asp
245

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<210> 7

<211> 1421

<212> DNA

<213> Homo sapiens

<220>

<221> exon

<222> (1)...(208)

<223> Zacrp5 exon 1

<221> intron

<222> (209)...(870)

<223> Zacrp5 intron 1

<221> exon

<222> (871)...(1421)

<223> Zacrp5 exon 2

<400> 7

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cgggtgagtg acagggacct gtggaggggg gacctgtgga gggggctgcc tcgagtacgg 180
cccactataa acatcgaaat cctcaaaggt gagggcccgtg ggtgctgcct gcatgctccc 240
ccaccaggac ccaacagccc acagggagtg gggagcacct ggggcttggg aggaggggcg 300
ggaggggcac tctgagcacc agtgtctgcc ctggcagcgc tccctgcaca gggaccctg 360
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gtgctgagga tcttggggaa gggggccagg gttcctgaga tcccaaagt agcagcccct 480
tggaaggga gcctgggcag cccgcttgct ctgagacccc ttgacacggc tgcgctgtcc 540
cgaagctgta ctaaggttag gcttgggtag gaccttccca gccttctcat tctttaacac 600
ccaacgcaga ccgtagctgg ccctgaccac ccatgtcccc accctctcgg tggggacggc 660

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cttgccacag gccttggtct agccacacct ttggagaacg gcttctcccc atcttacaga 720
cgtggacgcg gagactggga gaggggccgt cacttgcaaa gagtgtgtcc ttacagtgc 780
ccttgagccc cagcccctgg cctgggtgct ggaatggggg aggcctgccc agcccggccc 840
cgaccctggt ctttcgtttg tcccctgcag gtgagaaggg tgaggccggc gtccgaggtc 900
gggccggcag gagcgggaaa gaggggcccg caggcgcccg gggcctgcag ggccgcagag 960
gccagaaggg gcaggtgggg ccgcccggcg ccgcgtgccg acgtgcctac gccgccttct
1020
ccgtggggccg ggcgcagggc ctgcacagct ccgaccactt ccaggcgggtg cccttcgaca
1080
cggagctggt gaacctggac ggcgcttctg acctggccgc gggccgcttc ctctgcacgg
1140
tgccggcggt ctacttcctc agcctcaacg tgcacacctg gaactacaag gagacctacc
1200
tgcacatcat gctgaaccgg cggcccgcgg ccgtgctcta cgcgagagccc agcgagcgca
1260
gcgtcatgca ggcccagagc ctgatgctgc tgctggcggc gggcgacgcc gtctgggtgc
1320
gcatgttcca ggcgcaccgg gacaacgcca tctacggcga gcacggagac ctctacatca
1380
ccttcagegg ccacctggtc aagccggccg ccgagctgta g
1421

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<210> 8

<211> 31

<212> PRT

<213> Artificial Sequence

<220>

<223> Clq aromatic motif

<221> VARIANT

<222> (2)...(6)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (7)...(7)

<223> Xaa is asparagine or aspartic acid

<221> VARIANT

<222> (8)...(11)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (12)...(12)

<223> Xaa is phenylalanine, tyrosine, tryptophan or leucine

<221> VARIANT

<222> (13)...(18)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (20)...(24)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (26)...(26)

<223> Xaa is any amino acid residue

<221> VARIANT

<222> (28)...(28)

<223> Xaa is any amino acid residue

<221> VARIANT

<222> (30)...(30)

<223> Xaa is any amino acid residue

<221> VARIANT
 <222> (31)...(31)
 <223> Xaa is phenylalanine or tryrosine

<400> 8
 Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 10 15
 Xaa Xaa Phe Xaa Xaa Xaa Xaa Xaa Gly Xaa Tyr Xaa Phe Xaa Xaa
 20 25 30

<210> 9
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Degenerate oligonucleotide primer

<221> variation
 <222> (1)...(17)
 <223> Each N is independently A, T, G or C

<400> 9
 msgngnntnt aytwyyt 17

<210> 10
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Degenerate oligonucleotide sequence

<221> variation
 <222> (1)...(17)
 <223> Each N is independently A, T, G or C

<400> 10
 srnganvvng tntggbt 17

<210> 11
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Degenerate oligonucleotide primer

<221> variation
 <222> (1)...(17)
 <223> Each N is independently A, T, G or C

<400> 11
 rynttywsng gnywyyt 17

<210> 12
 <211> 756
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Degenerate nucleotide sequence encoding the
 polypeptide of SEQ ID NO:2

<221> variation
 <222> (1)...(756)
 <223> Each N is independently T, A, G or C

<400> 12
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 ytnccnmgnm gncntgygt ncaytgytgy mgncngcnt ggccnccngg nccntaygcn 120
 mgngtnwsng aymnggayyt ntggmgnggn gayytnntggm gnggnytncc nmngntnmgn 180
 ccnacnatha ayathgarat hytnaarggn garaarggng argcnggngt nmngggnmgn 240
 gcnggnmgmw snggnaarga rggncnccn ggngcnmgng gnytnargg nmgnmgnggn 300
 caraarggnc argtnggncc nccnggngcn gcntgymgnm gngcntaygc ngcnttywsn 360
 gtnggnmgnm gngarggnyt ncaywsnwsn gaycayttyc argcngtncc nttygayacn 420
 garytngtna ayytngaygg ngcnttygay ytnngcngcng gnmgnnttyt ntgyacngtn 480
 ccngngntnt ayttyytnws nytnaaygtn cayacntgga aytayaarga racntayytn 540
 cayathatgy tnaaymgngm nccngcngcn gtntyntayg cncarccnws ngarmgnwsn 600
 gtnatgcarg cncarwsnyt natgytnytn ytnngcngcng gngaygcngt ntgggtnmgn 660
 atgttycarm gngaymgnga yaaygcnath tayggngarc ayggngayyt ntayathacn 720
 ttywsnggnc ayytngtnaa rccngcngcn garytn 756

<210> 13
 <211> 12
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Representative contig

<400> 13
 atggcttagc tt 12

<210> 14
 <211> 12
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Representative contig

<400> 14
 tagcttgagt ct 12

<210> 15
 <211> 12
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Representative contig

<400> 15
 agccatcagc tg 12